APPENDIX

Amendments:

IN THE SPECIFICATION

On page 16, the paragraph beginning at line 5 is amended as follows:

5' C TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT CCC CGC CCC TTC GTC GTC CTC CTT CTC CCC CTC GCC AGC CCG GGC GCC CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGC GCG TCC CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG CCC CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC AC 3' (SEQ ID NO:13)

IN THE CLAIMS:

12. A diagnostic kit for the detection of SNP haplotypes (CC/GT) comprising at least one [primer and at least one probe] nucleic acid consisting of a nucleic acid selected from the group consisting of SEQ ID NO: [1 to 12] 1-12.

14. A method for predicting [the susceptibility] a risk of an individual to human spinocerebellar ataxia 2 (SCA2) disease, said method comprising:

a) amplifying genomic DNA of said individual using oligonucleotide primers [for PCR amplification of] to the CAG repeat-containing region of exon 1 of human SCA2 gene to obtain an amplified PCR product;

b) [sequencing the amplified PCR product and] identifying the nucleotides present at the polymorphic sites at nucleotides 107 and 178 of SEQ ID NO: 13 [sequence variations computationally by comparing the product with an established normal sequence for human SCA2 gene to determine whether said individual has a CC or GT haplotype]; and

c) predicting the risk [or susceptibility] of the individual to SCA2 disease based [on] upon the haplotype present at the polymorphic sites at [nucleotide position 481 and 552] nucleotides 107 and 178 of SEQ ID NO:13, wherein a G at position 107 of SEQ ID NO:13 and a T at position 178 of SEQ ID NO: 13 haplotype is indicative of a lower risk of SCA2 disease, and wherein a C at position 107 of SEQ ID NO:13 and a C at position 178 of SEQ ID NO:13 haplotype is indicative of an increased risk for SCA2 [in the individual tested, a GT haplotype being at low risk and a CC haplotype at high risk for the] disease.